



p53Ex8-9L 5'CAC GCT ATC CCG TTA GAC ATC TTA GTA ATT GAG GTG CGT GTT TGT GCC TGT C 3' (SEQ. ID. NO. 7)

p53Ex8-10R 5'CTG GGA GAG ACC GGC GCA CAT TAC TAC ATA GTG CGG TAG TTG GC 3' (SEQ. ID. NO. 8)

SODEx-3-11L 5'CAC GCT ATC CCG TTA GAC ATC TGT ACC AGT GCA GGT CCT CAC TTT AAT C 3' (SEQ. ID. NO. 9)

SODEx-3-12R 5'CTC TAT CCA GAA AAC ACG GTG GGC CGC TAC ATA GTG CGG TAG TTG GC 3' (SEQ. ID. NO. 10)

PCR Primers:

ZipALg1F 5' Fam-GGA GCA CGC TAT CCC GTT AGA C 3' (SEQ. ID. NO. 11) (T_m = 71°C)

ZipBLg2R 5' CGC TGC CAA CTA CCG CAC TAT G 3' (SEQ. ID. NO. 12) (T_m = 72°C) (SEQ. ID. NO. 12)

(Underlined sequences are common between LDR probes and ZipALg1F or the complement of ZipBLg2R.)

At page 84, Table 9:

Table 9 - LDR Oligonucleotide Sequences

Locus	Allele-Specific Oligonucleotide (5'-->3')	Common Oligonucleotide (5'-->3')
1	FAM-AGCTTCAATGATGAGAACCTGC (SEQ. ID. NO. 13) TET-AGCTTCAATGATGAGAACCTGT (SEQ. ID. NO. 15)	P-GCATAGTGGTGGCTGACCTGTT <u>CATAT</u> (SEQ. ID. NO. 14)
2	FAM-CTCCATGGGCCCAGCC (SEQ. ID. NO. 16) TET-CTCCATGGGCCCAGCT (SEQ. ID. NO. 18)	P-AGCACTGGTGGCCTGTGAG (SEQ. ID. NO. 17)
3	FAM-GGGGACAGCCATGCACTGA (SEQ. ID. NO. 19) TET-GGGGACAGCCATGCACTGC (SEQ. ID. NO. 21)	P-GCCTCTGGTAGCCTTTCAACCATA (SEQ. ID. NO. 20)
4	FAMTTAGAAATCATCAAGCCTAGGTCAT (SEQ. ID. NO. 22) TET-TTAGAAATCATCAAGCCTAGGTCAG (SEQ. ID. NO. 24)	P-CACCTTTTAGCTTCCTGAGCAATGAT (SEQ. ID. NO. 23)
5	HEX-GGTTGTATTTGTCACCATATTAATTA (SEQ. ID. NO. 25) HEX-ATGGTTGTATTTGTCACCATATTAATTG (SEQ. ID. NO. 27)	P-ATTTTCTCTATTGTTTTCATCTTTCAGGA (SEQ. ID. NO. 26)
6	FAM-GGGCCAAGAAGGTATCTACCA (SEQ. ID. NO. 28) TET-GGGCCAAGAAGGTATCTACCG (SEQ. ID. NO. 30)	P-ATAGTGTCTATTAGGCATTGAAAATGTGTAT (SEQ. ID. NO. 29)
7	FAM-ACACAGCAGCTTACTCCAGAGG (SEQ. ID. NO. 31)	P-TCAAGTCCAAGGCCATTGGCTTATA (SEQ. ID. NO. 32)

- TET-ACACAGCAGCTTACTCCAGAGA (SEQ. ID. NO. 33)
- 8 FAM-CCAGCAAAGAGAAAAGAAGGG (SEQ. ID. NO. 34) P-CCCCAGAAATCACAGGTGGGCTAT (SEQ. ID. NO. 35)
- TET-CCAGCAAAGAGAAAAGAAGGA (SEQ. ID. NO. 36)
- 9 FAM-ATGATATTAGAGCTCACTCATGTCCA (SEQ. ID. NO. 37) P-TCAGTTTGAAAAAGACAAAGAATTCTTT (SEQ. ID. NO. 38)
- TET-ATGATATTAGAGCTCACTCATGTCCG (SEQ. ID. NO. 39)
- 10 HEX-TGCTGTCTTCCAGGAATCTGTT (SEQ. ID. NO. 40) P-CAACTCTCTCGAAGCCATGTTACAA (SEQ. ID. NO. 41)
- HEX-ATTGCTGTCTTCCAGGAATCTGTG (SEQ. ID. NO. 42)
- 11 HEX-GGACATAGTGACCGTGCAGGTC (SEQ. ID. NO. 43) P-CTTCCCCAGTGTGAGTGCCGTA (SEQ. ID. NO. 44)
- HEX-ATGGACATAGTGACCGTGCAGGTT (SEQ. ID. NO. 45)
- 12 HEX-CTATGACACCGTCATCAGCAGG (SEQ. ID. NO. 46) P-GACATCCAGGCCCCCGAC (SEQ. ID. NO. 47)
- HEX-TACTATGACACCGTCATCAGCAGA (SEQ. ID. NO. 48)

The allele-specific oligonucleotides are 5' end labeled with either FAM, TET, or HEX. All the common oligonucleotides are phosphorylated at the 5' end. Underline denotes tails that are not complementary to the target sequence. LDR primer sets were designed in two ways: (i) allele-specific primers were of the same length but contained either FAM or TET label; or (ii) the allele-specific primers were both labeled with HEX but differed in length by two bases.

At page 88, Table 11:

TABLE 11 - Primary PCR Primer Sequences

Number	Primer
Name	(5'-->3')
1	F <u>GGAGCACGCTATCCCGTTAGACAGCCAAGGGGAACCCTGAGAG</u> (SEQ. ID. NO. 49)
	R <u>CGCTGCCAACTACCGCACTATGATCGTGGTCGAGGTGGTCACCATC</u> (SEQ. ID. NO. 50)
2	F <u>CCTCGTTGCGAGGCGTATTCTGTATTTCTCTTCTGTAAAAGGGAAGTTTGT</u> (SEQ. ID. NO. 51)
	R <u>GCGACCTGACTTGCCGAAGAACATGTCCCATCTCTCTACCTGATAC</u> (SEQ. ID. NO. 52)
3	F <u>GGAGCACGCTATCCCGTTAGACTAAAGATCTGTCTTGCGTCCCAGTCA</u> (SEQ. ID. NO. 53)

- R CGCTGCCAACTACCGCACTATGTATCAATTTTGCAGAGCTTAGATGGAATG (SEQ. ID. NO. 54)
- 4 F CCTCGITGCGAGGCGTATTCTGTAGCACTTGTGATCATGGTTTTAGAAATC (SEQ. ID. NO. 55)
- R GCGACCTGACTTGCCGAAGAACTATCGTATTTGATGATCCTCATAAAGTTG (SEQ. ID. NO. 56)
- 5 F GGAGCACGCTATCCCGTTAGACATCAGCCACTTGGAAGGAGCAAAC (SEQ. ID. NO. 57)
- R CGCTGCCAACTACCGCACTATGATGGACCATGGCTGAGTCTCCTTTAG (SEQ. ID. NO. 58)
- 6 F CCTCGITGCGAGGCGTATTCTGAACCAACACGGAGAAGCATTGTTTTTC (SEQ. ID. NO. 59)
- R GCGACCTGACTTGCCGAAGAACTATTAGCCTCAATCCTCATACTGACCTCTAC (SEQ. ID. NO. 60)
- 7 F GGAGCACGCTATCCCGTTAGACATCTCCTAACATCTATGTACTGGATTATCTAAATG (SEQ. ID. NO. 61)
- R CGCTGCCAACTACCGCACTATGATCTTACTCAAGTAATCACTCACCAGTGTTG (SEQ. ID. NO. 62)
- 8 F CCTCGITGCGAGGCGTATTCTGAATGAGTCAAATTGGCCTGGACTTG (SEQ. ID. NO. 63)
- R GCGACCTGACTTGCCGAAGAACTTAATTCCCGTGAGAAGGGAGATG (SEQ. ID. NO. 64)
- 9 F CCTCGITGCGAGGCGTATTCTGAAGGATCTGGATGAAGCCATTCTAAAC (SEQ. ID. NO. 65)
- R GCGACCTGACTTGCCGAAGAACTTGAAAAAGGTATTATAAGCAGAGAAAAGATG (SEQ. ID. NO. 66)
- 10 F GGAGCACGCTATCCCGTTAGACAGGACCGCAAAGGCTTTCATC (SEQ. ID. NO. 67)
- R CGCTGCCAACTACCGCACTATGTAGACCCAGGCTGTACCCAATTAG (SEQ. ID. NO. 68)
- 11 F CCTCGITGCGAGGCGTATTCTGATCGGGCGCTGGGCTTCAC (SEQ. ID. NO. 69)
- R GCGACCTGACTTGCCGAAGAACATCAGATGCCGCACTCCAAGAAG (SEQ. ID. NO. 70)
- 12 F GGAGCACGCTATCCCGTTAGACATAAGAGCCCACGGCGTCTCTTC (SEQ. ID. NO. 71)
- R CGCTGCCAACTACCGCACTATGTAAGAGACAGTGCCCAGGACAGAGTC (SEQ. ID. NO. 72)
- ZipALg1 F GGAGCACGCTATCCCGTTAGAC (SEQ. ID. NO. 73)
- ZipBLg2 R CGCTGCCAACTACCGCACAT G (SEQ. ID. NO. 74)
- ZipCLg3 F CCTCGT GCGAGGCGTATTCT G (SEQ. ID. NO. 75)

B3 ZipDLg4 R GCGACCTGACTTGCCGAAGAAC (SEQ. ID. NO. 76)

1
Solid underline denotes the ZipALg1 and ZipBLg2 sequences. Dotted underline denotes the ZipCLg1 and ZipDLg2 sequences. Linker sequences are indicated in bold. F=forward, R=reverse
